

SEQUENCE LISTING

<110> GOODNOW JR., ROBERT A.
MARK, DAVID F.
MARTIN, MITCHELL L.
ROSINSKI, JAMES A.

<120> SEQUENCE #115 AS A TARGET FOR IDENTIFYING WEIGHT
MODULATING COMPOUNDS

<130> 21366 US1

<140> 10/735,991

<141> 2003-12-15

<150> 60/436,375

<151> 2002-12-23

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<170> PatentIn Ver. 3.3

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 Tyr Thr Trp Leu His Ala Leu Thr Phe Pro Ala Thr Ala Leu Ala Leu
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 195 200 205
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 Arg Glu Arg Cys Leu Glu Glu Gln Lys Arg Arg Arg Gln Arg Ala Thr
 225 230 235 240
 Lys Lys Ile Ser Thr Phe Ile Gly Thr Phe Leu Val Cys Phe Ala Pro
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 Tyr Val Ile Thr Arg Leu Val Glu Leu Phe Ser Thr Ala Pro Ile Gly
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 Thr Cys Gly Asn Leu Leu Cys Thr Val Val Asn Met Pro Leu Thr Leu
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 Leu Ala Ala Phe Leu Asp Thr Phe Leu Ala Ala Asn Ser Met Leu Ser
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 Met Ala Ala Leu Ser Ile Asp Arg Trp Val Ala Val Val Phe Pro Leu
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Ser Tyr Arg Ala Lys Met Arg Leu Arg Asp Ala Ala Phe Met Val Ala
 115 120 125
 Tyr Thr Trp Leu His Ala Leu Thr Phe Pro Ala Thr Ala Leu Ala Leu
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 Ser Trp Leu Gly Phe His Gln Leu Tyr Ala Ser Cys Thr Leu Cys Ser
 145 150 155 160
 Arg Arg Pro Asp Glu Arg Leu Arg Phe Ala Val Phe Thr Ser Ala Phe
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 His Ala Leu Ser Phe Leu Leu Ser Phe Ile Val Leu Cys Phe Thr Tyr
 180 185 190
 Leu Lys Val Leu Lys Val Ala Arg Phe His Cys Lys Arg Ile Asp Val
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 Ile Thr Met Gln Thr Leu Val Leu Leu Val Asp Ile His Pro Ser Val
 210 215 220
 Arg Glu Arg Cys Leu Glu Glu Gln Lys Arg Arg Arg Gln Arg Ala Thr
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 Lys Lys Ile Ser Thr Phe Ile Gly Thr Phe Leu Val Cys Phe Ala Pro
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 Tyr Val Ile Thr Arg Leu Val Glu Leu Phe Ser Thr Ala Pro Ile Asp
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<213> Homo sapiens

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Gly Val Ser Leu Leu Ser Asn Ala Leu Val Leu Leu Cys Leu Leu His
      20              25              30

Ser Ala Asp Ile Arg Arg Gln Ala Pro Ala Leu Phe Thr Leu Asn Leu
      35              40              45

Thr Cys Gly Asn Leu Leu Cys Thr Val Val Asn Met Pro Leu Thr Leu
      50              55              60

Ala Gly Val Val Ala Gln Arg Gln Pro Ala Gly Asp Arg Leu Cys Arg
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Leu Ala Ala Phe Leu Asp Thr Phe Leu Ala Ala Asn Ser Met Leu Ser
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Met Ala Ala Leu Ser Ile Asp Arg Trp Val Ala Val Val Phe Pro Leu
      100             105             110

Ser Tyr Arg Ala Lys Met Arg Leu Arg Asp Ala Ala Leu Met Val Ala
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Tyr Thr Trp Leu His Ala Leu Thr Phe Pro Ala Ala Ala Leu Ala Leu
      130             135             140

Ser Trp Leu Gly Phe His Gln Leu Tyr Ala Ser Cys Thr Leu Cys Ser
      145             150             155             160

Arg Arg Pro Asp Glu Arg Leu Arg Phe Ala Val Phe Thr Gly Ala Phe
      165             170             175

His Ala Leu Ser Phe Leu Leu Ser Phe Val Val Leu Cys Cys Thr Tyr
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Leu Lys Val Leu Lys Val Ala Arg Phe His Cys Lys Arg Ile Asp Val
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[illegible]